30. The segment of claim 1, wherein the polymorphic site is at a position selected from the group consisting of 15043, 15067, 15110, 15119, 15136, 15217, 15244, 15301, 15431 and 15629.

31. The segment of claim 1, wherein the polymorphic site is at a position selected from the group consisting of 15734, 15784, 15849, 15883, 15902, 16093, 16111, 16114, 16124 and 16126.

32. The segment of claim 1, wherein the polymorphic site is at a position selected from the group consisting of 16129, 16145, 16148, 16264, 16278, 16290, 16318, 16319, and 16354.

33. The segment of claim 1, wherein the polymorphic site is at a position selected from the group consisting of 16362, 16390 and 16519.

REMARKS

Table 1 has been amended to correct a discrepancy in base numbering between the present application and the reference mitochondrial sequence of Anderson et al. In brief, the mitochrondrial sequence begins in accordance with convention at nucleotide 1. By contrast, the nucleotide sequence in previous table 1 began with the first nucleotide being numbered as zero. Accordingly, in the amended table, each position has been increased by one to conform to the numbering system of Anderson et al. The error was an obvious one when the reference nucleotides shown in Table 1 are compared with nucleotides at the corresponding positions of the Anderson et al. sequence. Moreover, the application specifically discloses that applicants intended to use the same numbering as Anderson et al. (see specification at p. 10, lines 8-13). Therefore, the correction does not constitute new matter. The new dependent claims specify groups of about ten polymorphic positions from those listed in Table 1 (as amended).

35 USC 112, second paragraph

Dependency of claims 5-7 has been corrected has been corrected. Dependency of claim 8 is corrected by the correction to claim 7.

Claims 1 and 9 have been amended to recite "perfect" complement as requested by the Examiner. It is submitted that the specification inherently discloses perfect complements of the sequences of Table 1. Mitochondrial DNA is inherently double stranded, and as with other double-stranded sequences, mitochrondrial DNA is conventionally represented by showing only a single strand, it being understood that the other strand is the perfect complement of the strand presented.

Rejection of claim 4 under 102(b) over Sigma Chemical Catalog

The Examiner says that an oligonucleotide in the Sigma catalog would hybridize notwithstanding a one base mismatch to a segment overlapping position 315. This rejection has been rendered moot by specifying that the allele specific oligonucleotide is perfectly complementary to its target strand (see, p. 11, first paragraph for support).

Attached hereto is a marked-up version of the changes made to the specification by the amendment. The attached page is captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

The table on pages 30-33 has been amended as follows:

Table 1

pos	rbase	asn_base	HA001_v_mt2	HA002_v_mt2	HA004_v_mt2	HA007_v_mt2	IB013_v_mt2	IGF002_v_mt2	IGF005_v_mt2	IGF007_v_mt2	HA001_v_mt2	YR019
634	C	c	C	C	T	C	C	C	C	C	C	C
723	G	a	G	G	A	G	G	G	G	G	G	G
923	A	a	A	g	G	G	A	A	A	A	A	A
1812	C	c	T	T	c	T	c	t	C	C	C	C
1945	T	t	c	C	t	C	t	c	T	C	C	C
2345	G	a	A	A	g	A	a	A	A	A	A	A
2467	G	g	G	G	A	G	a	G	G	G	G	G
2967	A	a	A	A	A	A	G	A	A	A	A	A
3156	G	g	G	G	G	G	A	G	G	G	G	G
3245	C	c	C	T	C	T	C	C	C	C	C	C
6623	G	a	A	A	A	A	A	A	A	A	A	A
67980	T	t	T	C	T	C	T	T	T	T	T	T
7089	G	g	A	A	G	A	G	A	G	G	G	G
7689	G	g	A	a	a	a	a	A	G	A	A	a
8245	T	t	T	T	A	T	A	T	T	T	T	T
10178	G	g	A	A	A	A	A	A	G	A	A	A
103940	T	t	T	T	T	C	T	T	T	T	T	T
10478	C	c	C	C	T	C	C	C	C	C	C	C
14412	G	g	A	A	G	A	G	A	G	G	G	G
17056	C	c	T	C	C	C	C	T	C	C	C	C
17356	G	a	A	A	A	A	A	A	A	A	A	A
23578	A	a	G	A	A	A	A	G	A	A	A	A
24156	T	t	t	t	T	t	T	A	T	n	t	t
27578	G	g	G	G	A	G	A	G	G	G	G	G
27889	C	c	C	C	C	C	C	C	C	T	T	T
28845	T	t	T	T	C	T	C	T	T	T	T	T
300910	G	g	G	G	G	G	G	G	G	G	G	A
3199200	T	t	T	A	T	A	T	T	T	T	T	T
33356	T	t	T	T	T	T	T	T	T	T	C	T
33367	G	g	G	A	G	G	G	G	G	G	G	G
344950	C	c	C	C	C	C	C	C	T	C	C	C
35156	C	c	C	C	A	C	C	C	C	C	C	C
35934	C	c	T	T	T	t	c	T	C	T	T	T
36478	C	c	T	C	C	C	C	C	C	C	C	C
36656	G	g	G	G	G	G	A	G	G	G	G	G
37445	G	g	G	A	G	G	G	G	G	G	G	G
38656	T	t	T	T	C	T	T	T	T	T	T	T
39178	G	g	G	G	G	G	G	G	G	A	A	G
41034	A	a	G	G	G	G	G	G	A	G	G	G
41578	A	a	G	A	A	A	A	G	A	A	A	A
42478	C	t	T	T	T	T	T	T	T	T	T	T

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pos	rbase	asn_base	HA001_v_mt2	HA002_v_mt2	HA004_v_mt2	HA007_v_mt2	IB013_v_mt2	IGF002_v_mt2	IGF005_v_mt2	IGF007_v_mt2	HA001_v_mt2	YR019
43112	C	c	C	C	T	C	C	C	C	C	C	C
45856	T	t	T	T	C	T	T	T	T	T	T	T
47667	A	a	G	A	A	A	A	G	A	A	A	A
48234	G	a	A	A	A	A	A	A	A	A	A	A
49667	T	t	T	T	T	C	T	T	T	T	T	T
50267	C	c	T	C	C	C	C	T	C	C	C	C
50956	T	t	T	T	C	T	T	T	T	T	T	T
51467	G	g	G	G	G	G	G	G	G	G	A	G
52301	G	g	G	G	A	G	G	G	G	G	G	G
52512	G	g	G	G	G	G	G	G	G	G	G	A
52845	A	a	A	A	A	A	A	A	A	g	G	A
53301	C	c	A	C	C	C	C	A	C	C	C	C
545960	G	g	G	G	A	G	G	G	G	G	G	G
56023	C	c	C	C	T	C	C	C	C	C	C	C
57723	G	g	G	G	G	G	G	G	A	G	G	G
58134	T	t	C	T	T	T	T	C	T	T	T	T
58223	A	a	A	A	A	G	A	A	A	A	A	A
59112	C	c	T	C	C	C	C	C	C	C	C	C
60701	T	t	T	T	T	T	C	T	T	T	T	T
614950	G	g	G	G	G	G	A	G	G	G	G	G
62367	C	c	C	C	C	C	C	C	T	C	C	C
62523	T	t	T	T	T	T	C	T	T	T	T	T
65267	G	a	A	A	A	A	A	A	A	A	A	A
66134	T	t	C	T	T	T	T	C	T	T	T	T
66623	A	a	A	A	A	A	A	A	A	A	A	G
67123	C	c	T	C	C	C	C	T	C	C	C	C
68056	A	a	G	A	A	A	A	G	A	A	A	A
68267	T	t	T	C	T	T	T	T	T	T	T	T
68745	C	c	C	C	C	C	C	C	C	A	C	C
71456	A	a	A	A	G	A	G	A	A	A	A	A
71745	T	t	T	T	T	T	T	T	T	C	C	C
72556	C	c	T	T	T	T	T	T	C	T	T	T
72734	C	c	C	C	C	C	C	C	C	T	T	T
73889	T	t	T	T	T	T	C	T	T	T	T	T
75178	A	a	A	n	A	G	a	a	A	N	A	A
75201	G	g	A	c	A	G	g	g	G	A	A	A
76234	T	t	A	A	T	A	T	A	T	T	T	T
77701	A	a	A	A	A	A	A	A	A	G	G	g
80267	A	g	G	G	G	G	A	G	G	G	G	G
807980	C	c	T	C	C	C	C	T	C	C	C	C
82056	G	g	A	A	G	A	G	A	G	A	A	A
83867	G	g	A	G	G	G	G	A	G	G	G	G
84278	C	c	C	C	T	C	C	C	C	C	C	C
84678	C	c	c	C	T	C	T	C	C	C	c	C
85023	T	t	C	T	T	c	T	C	T	T	T	T
85656	A	a	A	A	G	A	A	A	A	A	A	A
86545	C	c	C	C	T	C	T	C	C	C	C	C
87001	A	a	G	G	G	G	G	G	G	G	G	G
87834	A	a	A	A	A	A	G	A	A	A	A	A
87934	T	c	C	C	C	C	C	C	C	C	C	C
88534	G	g	G	G	G	G	G	G	G	G	G	A
88767	T	t	T	T	T	T	C	T	T	T	T	T

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pos	rbase	asn_base	HA001_v_mt2	HA002_v_mt2	HA004_v_mt2	HA007_v_mt2	IB013_v_mt2	IGF002_v_mt2	IGF005_v_mt2	IGF007_v_mt2	HA001_v_mt2	YR019
90412	C	c	C	C	T	C	C	C	C	C	C	C
90712	A	a	A	A	A	A	G	A	A	A	A	A
92201	A	a	G	G	A	G	A	G	A	G	G	G
93467	A	a	A	A	G	A	A	A	A	A	A	A
94489	C	c	C	C	C	C	C	C	T	C	C	C
98178	C	c	C	C	T	C	C	C	C	C	C	C
100301	T	t	T	T	T	T	C	T	T	T	T	T
101145	T	t	C	C	T	c	T	C	T	C	C	T
103201	T	t	T	T	T	T	C	T	T	T	T	T
103723	G	g	G	G	G	G	G	G	A	G	G	G
105856	G	g	G	G	g	G	A	G	G	G	G	G
106634	C	c	C	C	T	C	C	C	C	C	C	C
106878	G	g	G	G	A	G	A	G	G	G	G	G
107923	C	c	C	C	C	C	T	C	C	C	C	C
1080910	T	t	T	T	C	T	C	T	T	T	T	T
108278	T	t	T	T	T	T	C	T	T	T	T	T
108723	T	t	C	C	C	C	C	C	C	C	C	C
109145	T	t	T	T	C	T	T	T	T	T	t	T
111634	A	a	A	A	A	A	G	A	A	A	A	A
111756	A	g	G	G	A	G	G	G	G	G	G	G
116401	A	a	A	A	G·	A	A	A	A	A	A	A
116534	A	a	A	A	A	A	G	A	A	A	A	A
11799800	A	a	A	A	A	A	A	A	G	A	A	A
119134	G	g	G	G	A	G	G	G	G	A	A	A
119434	T	t	C	C	T	C	T	C	T	C	C	C
120067	A	g	G	G	A	G	G	G	G	G	G	G
120489	C	c	C	C	C	C	T	C	C	C	C	C
121145	C	c	C	C	C	C	T	C	C	C	C	C
122356	G	g	A	A	G	A	G	A	G	G	G	G
123534	T	t	T	T	T	T	T	T	T	T	T	C
124767	T	t	T	T	T	T	C	T	T	T	T	T
1271920	A	a	A	A	G	A	A	A	A	A	A	A
127767	A	a	G	A	A	A	A	A	A	A	A	A
1280910	A	a	A	A	A	A	G	A	A	A	A	A
129478	A	a	G	A	A	A	A	G	A	A	A	A
131045	A	a	A	A	G	A	G	A	G	A	A	A
131489	A	a	A	A	A	A	G	A	A	A	A	A
131834	T	t	T	T	T	C	T	T	T	T	T	T
132023	A	a	A	A	A	G	A	A	A	A	A	A
132756	A	a	A	A	G	A	A	A	A	A	A	A
134845	A	a	A	A	A	A	G	A	A	A	A	A
135056	C	c	C	C	T	C	t	C	C	C	C	C
1358990	G	g	a	A	G	A	G	A	G	A	A	A
1364950	C	c	t	t	t	t	T	T	C	T	T	t
137889	T	t	T	T	T	T	C	T	T	T	t	T
138023	A	a	A	A	A	A	A	A	A	g	G	g
139134	C	c	C	C	C	C	C	C	A	C	C	C
139578	G	g	G	C	G	C	G	G	G	G	G	G
139656	A	a	G	A	A	A	A	G	A	A	A	A
139994000	T	t	T	T	T	T	A	T	T	T	T	T
140589	A	a	G	A	A	A	A	G	A	A	A	A
141778	T	t	T	T	T	T	C	T	T	T	T	T

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pos	rbase	asn _base	HA001_ v_mt2	HA002_ v_mt2	HA004_ v_mt2	HA007_ v_mt2	IB013_ v_mt2	IGF002_ v_mt2	IGF005_ v_mt2	IGF007_ v_mt2	HA001_ v_mt2	YR019
143078	T	t	T	T	C	T	T	T	T	T	T	T
144067	C	c	T	C	C	C	C	T	C	C	C	C
1455960	G	g	G	G	G	G	A	G	G	G	G	G
145656	A	a	A	A	A	A	A	A	A	G	G	G
149101	C	c	C	C	C	C	T	C	C	C	C	C
150423	G	g	G	G	G	A	G	G	G	G	G	G
150667	T	t	T	T	T	T	C	T	T	T	T	T
1510910	G	g	A	A	G	A	G	A	G	G	G	G
151189	G	g	G	G	G	G	G	G	G	G	G	A
151356	C	c	C	C	T	C	C	C	C	C	C	C
152167	G	g	A	A	G	A	G	A	G	G	G	G
152434	A	a	A	A	A	A	A	A	A	G	G	A
153001	G	g	A	A	G	A	G	A	a	A	A	A
154301	G	g	G	G	A	G	G	G	G	G	G	G
156289	T	t	T	T	T	T	T	T	T	C	C	T
157334	G	g	G	G	G	G	G	G	G	G	G	A
157834	T	t	T	T	T	T	T	T	T	C	C	C
158489	C	c	C	T	C	T	C	C	C	C	C	C
158823	G	g	G	G	G	G	G	G	A	G	G	G
159012	A	a	A	A	A	A	A	A	G	A	A	A
160923	T	t	T	T	T	T	C	T	T	T	T	T
161101	T	c	C	C	C	C	C	C	C	C	C	C
161134	C	c	A	C	C	C	C	A	C	C	C	C
161234	T	t	t	T	T	T	T	T	C	T	T	T
161256	T	t	t	T	T	T	T	T	T	T	C	T
161289	G	g	A	G	A	G	G	G	G	G	G	G
161445	G	g	G	G	G	G	G	A	G	G	G	G
161478	C	c	C	C	T	C	C	C	C	C	C	C
162634	C	c	C	C	C	T	c	C	C	C	c	C
162778	C	c	T	T	C	T	t	T	T	t	T	T
1628990	T	c	C	C	C	C	t	C	C	t	c	c
163178	A	a	A	G	a	A	A	A	A	A	A	A
163189	A	g	G	G	g	G	G	G	G	G	G	G
163534	C	c	T	C	C	C	C	T	C	C	C	C
163612	C	t	T	T	C	T	T	T	C	T	T	T
1638990	G	g	A	a	G	a	G	A	G	A	A	A
165189	T	t	T	T	C	T	c	T	C	C	C	C

IN THE CLAIMS

1. (Amended) A segment of human mitochondrial DNA or RNA of between 10 and 100 bases including any one of the polymorphic sites shown in Ftable 1, wherein the polymorphic site within the segment is occupied by a base other than the base shown in Table 1, column 3 ("asn base") or the perfect complement of the segment.

4. (Amended) An allele-specific oligonucleotide that [hybridizes] is perfectly complementary to a segment of human mitochondrial nucleic acid or its perfect complement

including a polymorphic site shown in Table 1, column 1, wherein the polymorphic site within the segment is occupied by a base other than the base shown in Table 1, column 3 ("asn" base).

5. (Amended) The allele-specific oligonucleotide of claim [10] 4 that is a probe.

6. (Amended) The allele-specific oligonucleotide of claim [10] 4, wherein a central position of the probes aligns with the polymorphic site of the fragment.

7. (Amended) The allele-specific oligonucleotide of claim [10] 4 that is a primer.

9. (Amended) An isolated nucleic acid comprising a segment of at least 10 contiguous bases from SEQ ID NO: 30, or the perfect complement thereof, including a polymorphic site shown in Table 1, wherein the polymorphic site within the segment is occupied by a base other than the base shown in Table 1, column 3 ("asn base").